

LE BDD hFVIII
pXF8.61

THROMBIN

THROMBIN

A1 A2 R LE E A3 C1 C2

740 1649

APC APC

BEST AVAILABLE COPY

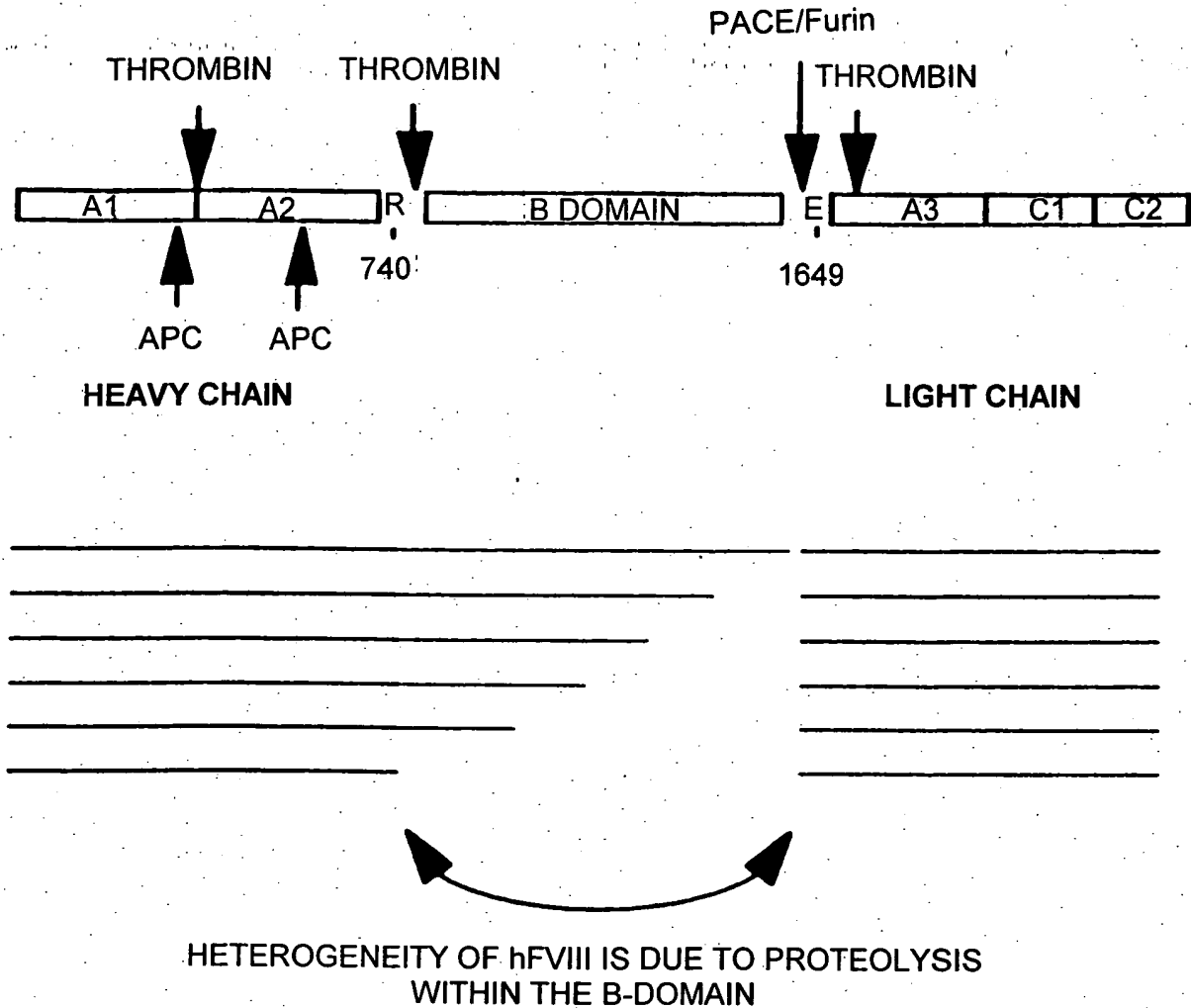


FIG. 2

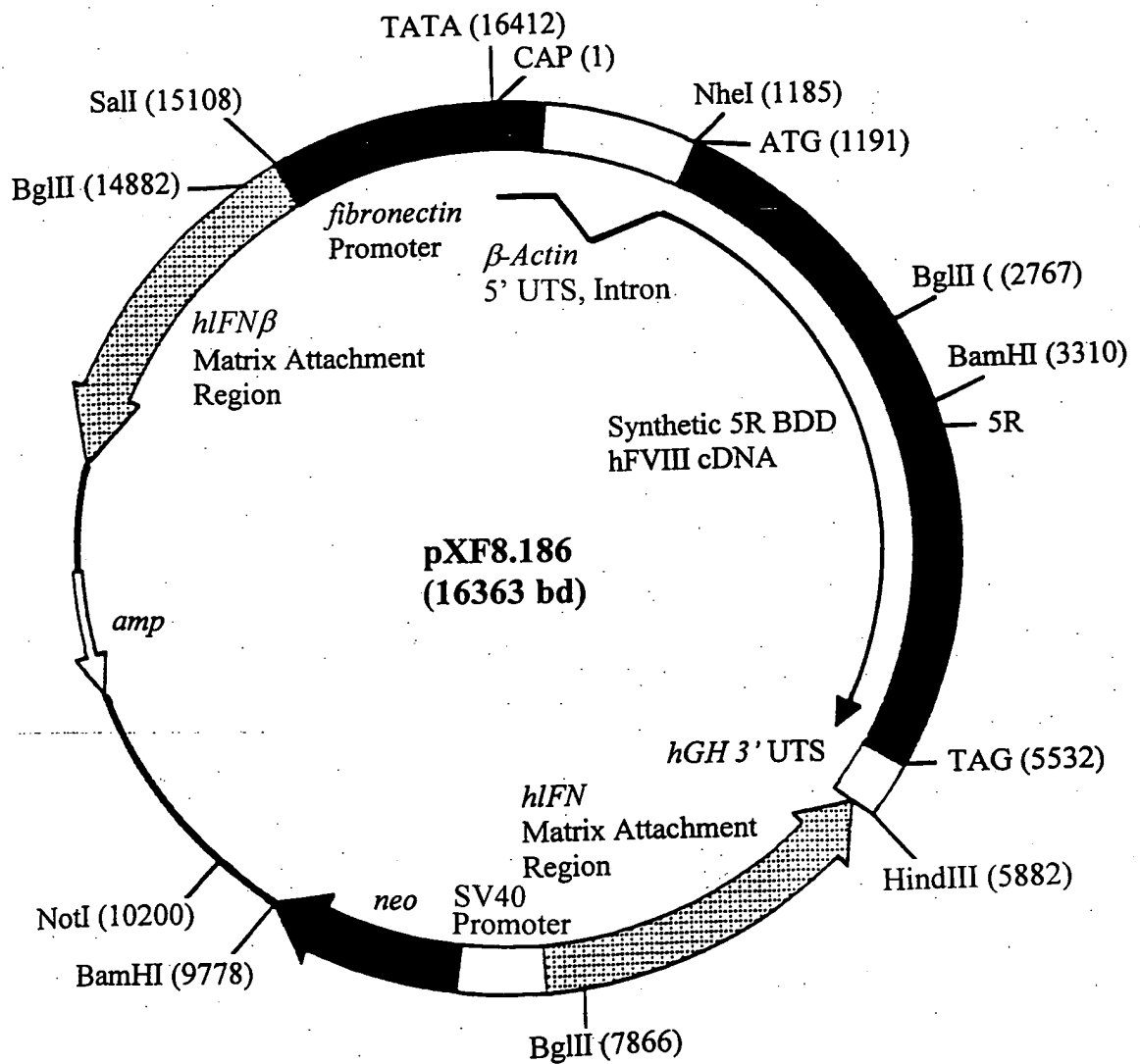


FIG. 3

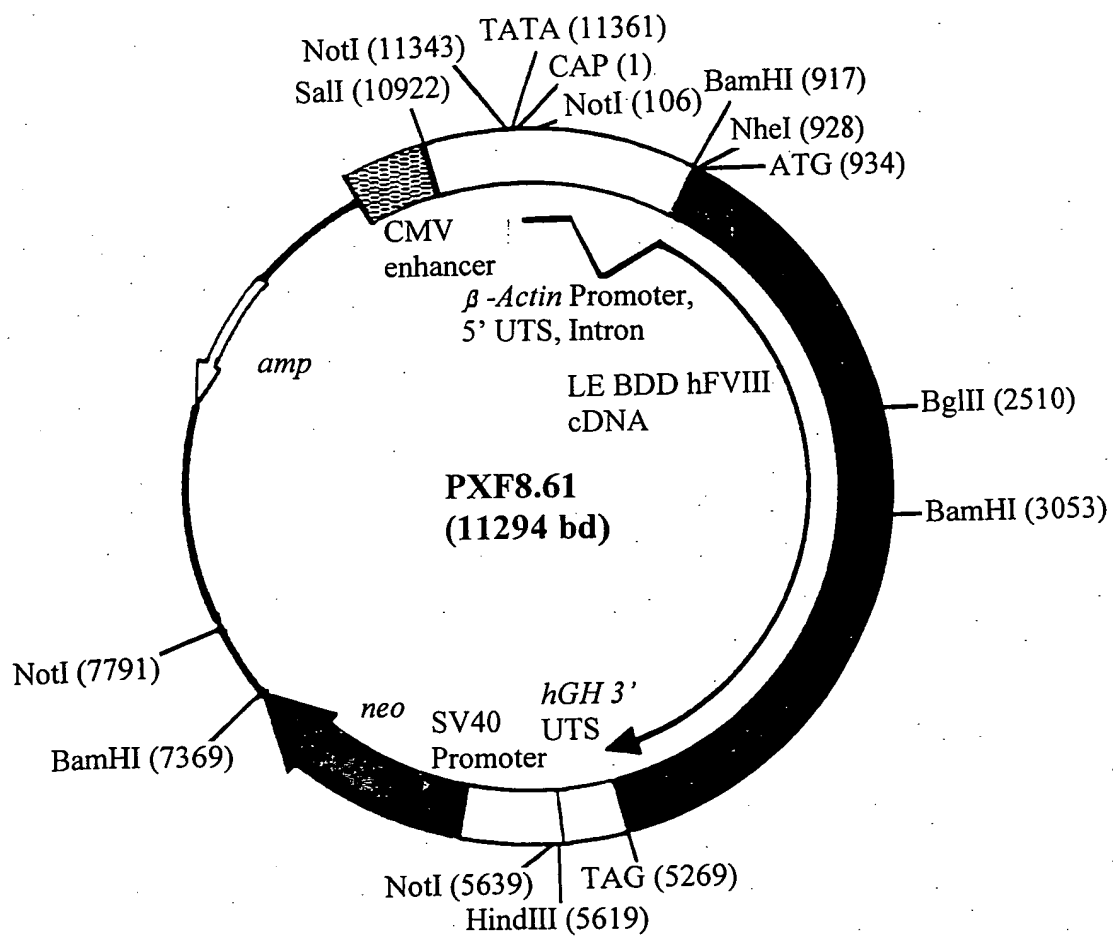


FIG. 4

Fragment A

EcoRI	NheI	AM1 Af1
GTAGAAATTCGTAGGCTAGCATGCAGATCGAGCTGAGCACCTGCTTCTCCTGTGCTGCTGCGCTTCTGCG		
CATCTTAAGCATCCGATCGTAGCTAGCTCGACTCGTGGACGAAGAAGGACACGACGACGCGAAGACG		
		AM1 Ar3
TTCAGCGCCACCCG	3' OH 5' P	
CCGCTACTACCTGGGCGCCGTGGAGCTGAGCTGG		
AAGTCGGGTGGG	5' P 3' OH	
GGCGATGATGGACCCCGCGCACCTCGACTCGACC		AM1 Ar2
		AM1 Af2
GGCGAGCTGCCCGTGGACGCCCGCTTCCCCCGCGTGCCCAAGAGCTTCC		
CCCCGCTGACGGGCACCTGCGGGCGAAGGGGGGCGCACGGGTTCTCGAAGG	5' P 3' OH	
		AM1 Af3
GGTGTAAGAAGAC	3' OH 5' P	
CCTGTTCTGTTGAGTTACCGACCACTGTTCAACATCGCCAAAGCCCCCCCC		
CCACATGTTCTTCTG		AM1 Ar1
GGACAAAGCACCTCAAGTGGCTGGTGGACAAAGTTGTAGCGGTTCTGGGGCGGGGGG		
Apal	HindIII	
CTGGATGGGCGCTGTGGGCCCC		
GACCTACCCGGACGACCCGGGATGTTCGAAATG		

FIG. 5A

Fragment B

EcoRI	Apal	AM1 Bf1	
GTAGAAATTCGTAGGGGCCCCACCATCCAGGCCGAGGTGTACGACACCGTGGTGATCACCCCTGAAGAACATGGCCAG			
CATCTTAAGCATCCCCGGGTGGTAGGTCGGCTCCACATGCTGTGGCACCCACTAGTGGGACTTCTTGTAACCGGTC			
		AM1 Br3	
		3' OH 5' P	
CCACCCCGTGAGC	CTGCACGCCGTGGGCGTGAGCTACTG		
GGTGGGGCACTCG	GACGTGCGGCACCCCGCACTCGATGAC	AM1 Br2	
5' P 3' OH			3' OH 5' P
	AM1 Bf2		
CCAGCCAGCGCGAGAAGGAGGACGACAAAGGTGTTCCCGG	CGGCAGCCACACCTACGTGTGGCAGGTG		
GGTCGGTCGCGCTCTTCC	TGCTGTTCCACAAGGGGCC		
	5' P 3' OH		
	AM1 Bf3	PmII	HindIII
GAGAACGGCCCCCATGGCCAGCGACCCCTGTGCCTGACCTACAGCTACCTGAGCCACGTCGTACAAGCTTTAC			
CTCTTGCCGGGTACCGGTGCGCTGGGGGACACGGACTGGATGTCGATGGACTCGGTGCACGATGTTTCGAAATG			
AM1 Br1			

FIG. 5B

Fragment C

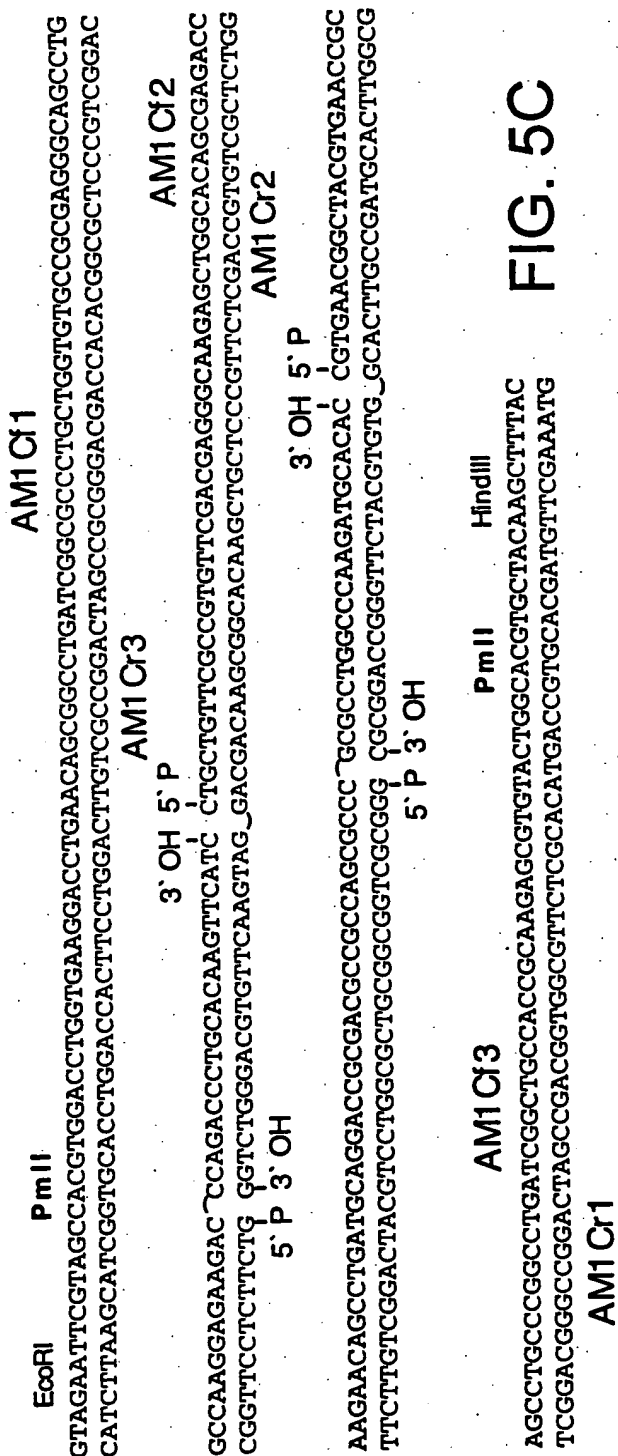


FIG. 5C

Fragment D

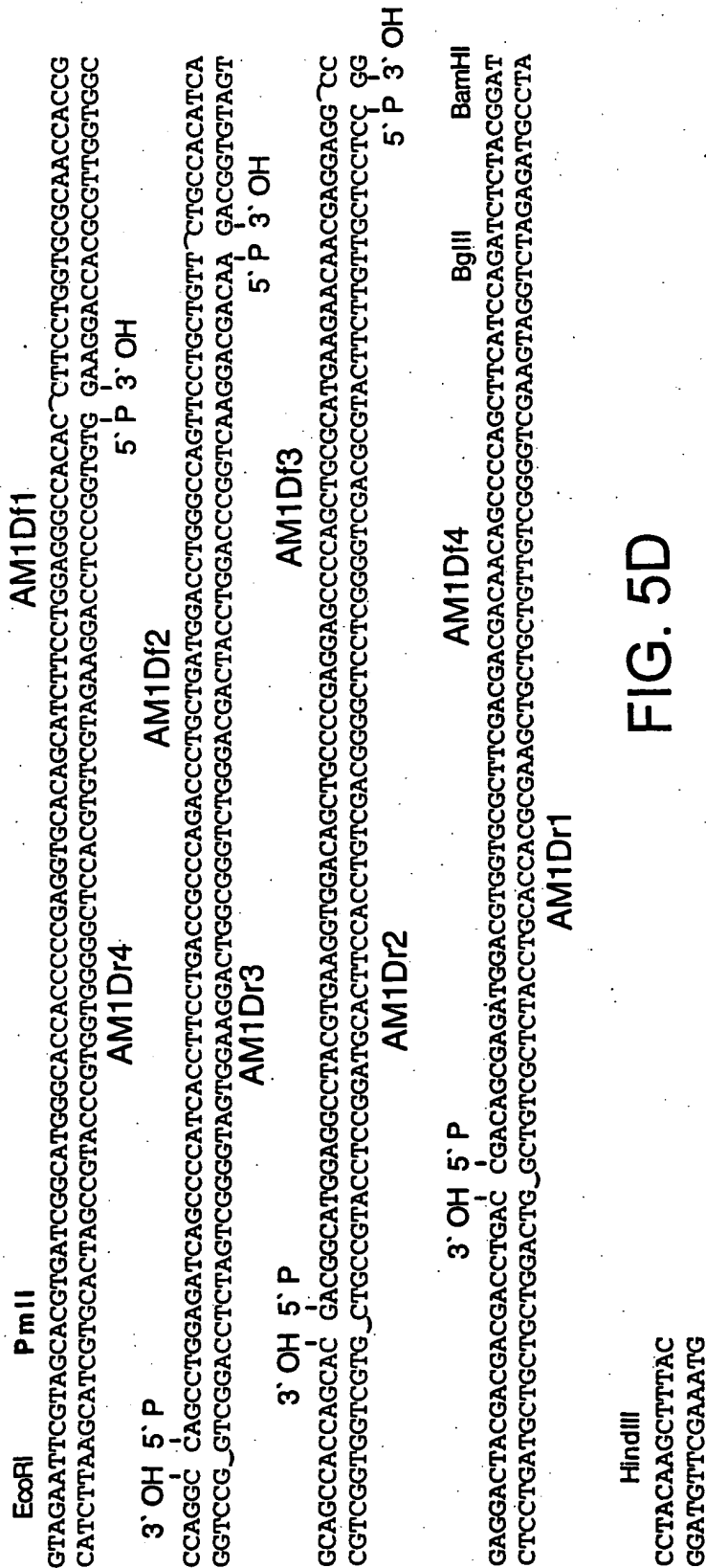


FIG. 5D

Fragment E

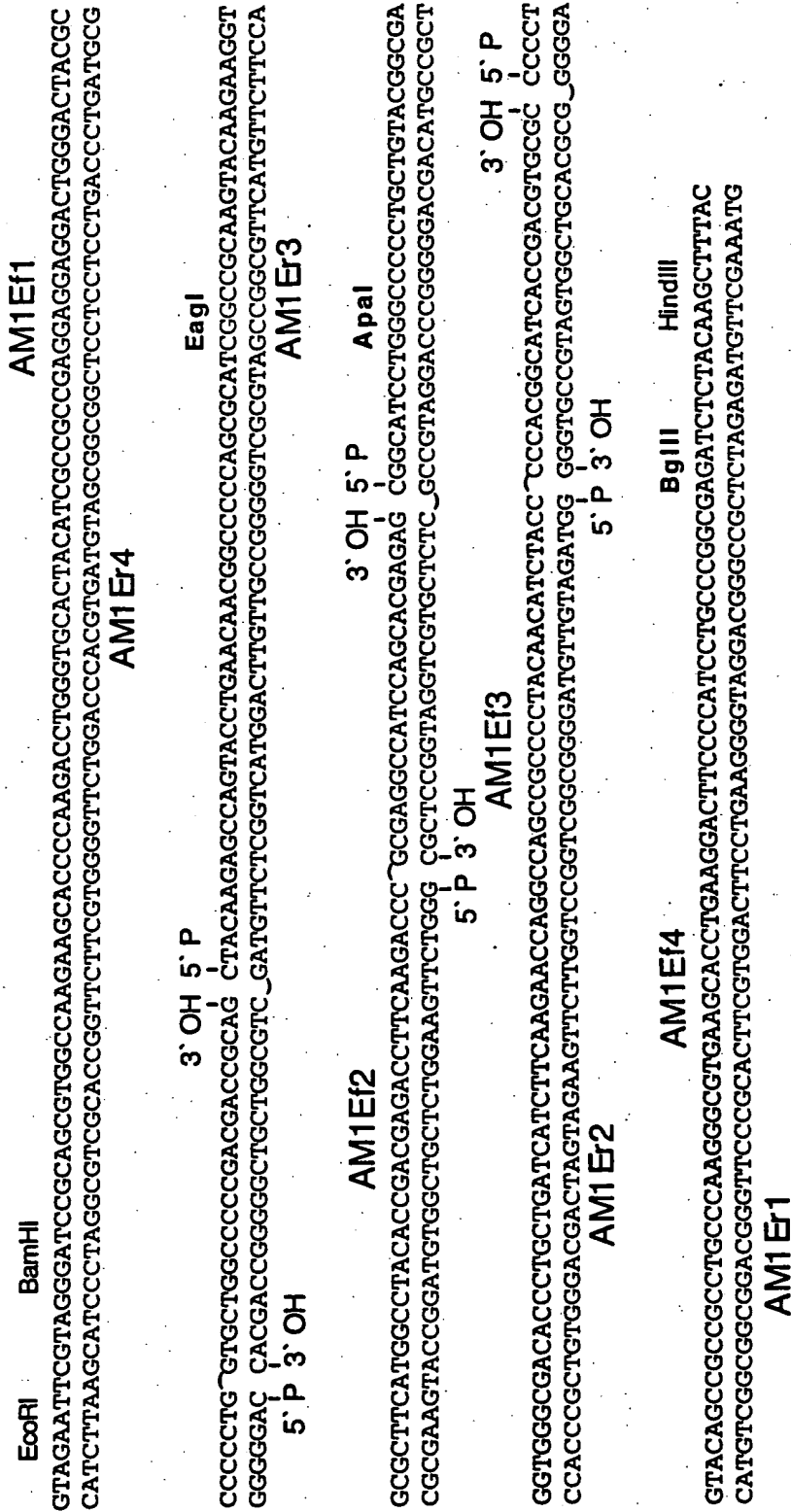


FIG. 5E

Fragment F

HindIII	KpnI		AM1 F1
G T A A G C T T G T A G G G T A C C A G C T G C G G T T C T C G T C G A A C A C G C T G A A C A G G A T C A C G T T G C T G C T T G C G C T C A T G A T C T G G T T G C C C A T T T C G A A C A T C C C A T G G T C G A C G C C A A G A G A G A G A C G T T G T G C G A C T T G T C C T A G T G C A A C G C G A A C A G C G G A G T A C T A G A C C A A C G G			
		AM1 Fr3	5' P 3' OH
3' OH 5' P		AM1 F2	
G		C G C T G G T C C A C G C T C T C C T T G T A G C A G A T C A G A G G G G C C G A T C A G C C C G C T G G C C A G G T C G C G C T C C A T G T T C A C T G A A G C T G	5' P 3' OH
C		G C G A C C A G G T G C G A G A G G A A C A T C G T C T A G T C G T C C C C C G G C T A G T C C G G C G A C C G G T C C A G C G C G A G G T A C A A G T G C T T C G A C	
		AM1 Fr2	
3' OH 5' P		AM1 F3	BglII
C T G T A G T A G C G G G T C A G		G C A G C G G G G T C G C T C T T G G T G G G G C C G T C C T C C A C G G T C A C G G T C C A C T T G T A C T T G A A G A T C T C T A C	
G A C A T C A T C G C C C A G T C		C G T C G C C C C C A G C G A A C C A C C C C G C A G G A G G T G C C A G T G C C A G G T G C C A C A T G A A C T T C T A G A G A T G	
		AM1 Fr1	
EcoRI			
G A A T T C T A C			
C T T A A G A T G			

FIG. 5F

Fragment G

EcoRI	KpnI	AM1Gf1
GTAGAATTCTGTAGGGTACCTGACCGAGAACATCCAGCGCTTCTGCCCCAACCCCGCGCGTGCAGCTGGAGGACCCCGAGTTCCAGGCCAG		
CATCTTAAGCATCCCATGGACTGGCTCTTGTAGTCCGGAAGGACCGGGTTGGGGCGCCGACGTCGACCTCCTGGGGCTCAAGGTCCGGTC		
		AM1Gr3
3' OH 5' P		
CAACAT	CATGCACAGCATCAACGGCTAC	AM1Gf2
GTGTGTA	GTACGGTGTCTGTAGTTGCCGATG_CACAAGCTGTCTGGACGTCGACTCGCACACGGACGTGCTCCACCGGATGACCATGTAGGACTC	
5' P 3' OH		AM1Gr2
3' OH 5' P		
CATCGCGCGCCAGACCGACTTCTGTAGCGTGTCTTTCAGC	GGCTACACCTTCAAGCACAAAGATG	
GTAGCCGCGGGTCTGGCTGAAGGACTCGCACAAAGATCG	CCGATGTGGAAGTTCGTGTCTTAC_CACATGCTCCTGTGGGACTGGGACAA	
5' P 3' OH		
AM1Gf3	BamHI	HindIII
CCCCTTACGGCGGAGACCGTGTTCATGAGCATGGAGAACCCCGCGCTGTGGATCCCTACAAGCTTTTAC		
GGGGAAGTCGCCCGCTCTGGCACAAAGTACTCGTACCTCTTGGGGCCGGACACCTAGGGATGTTCGAAATG		
AM1Gr1		

FIG. 5G

FIG. 5H

Fragment I

EcoRI	PmII	AM1 If1	
GTAGAAATTCGTAGCACGTGTCGCAACCGCGCCAGAGCGGCAGCGTCCCAAGTTCAAGAGGTGGTGTTCACGAGGTTTACCGACGGCAGCTTCACCCAG			
CATCTTAAGCATCGTGCACGACGCGTTGGCGGGTCTCGCCGTCCGACGGGGTCAAGTTCTTCCACCACAAAGGTCTCTCAAGTGGCTGCCGTG	AM1 Ir4		5' P 3' OH
		AM1 If2	BstEII
CCCCGTGTACCGC	Apal		
GGCGAGCTGAACGAGCACCTGGGCCCTGCTGGCCCCCTACATCCGCGCCGAGGTGGAGGACAAACATCATGTGACCCGTGCAGGAGTTCC			5' P 3' OH
GGGGACATGGCG	AM1 Ir3	AM1 If3	
CCGCTCGACTTGCTCGTGGACCCCGGACGACCCCGGGATGTAGGGCGGCTCCACCTCTGTTGTAGTACCACCTGGCACGTCTCTCAAGC			5' P 3' OH
3' OH 5' P			
CTGTTCTTCCACCATCTTCGAC		AM1 If4	KpnI
GAGACCAAGAGCTGGTACTTTCACCCGAGAACATGGAGCGCAACTGCCCGCCCCCTGCAACATCCAGATGGAGGACCCTCACC			
GACAAGAAGTGGTAGAAGCTG	AM1 Ir2		5' P 3' OH
CTCTGGTTCTCGACCATGAAGTGGCTCTTGTAACCTCGCGTTGACGCGCGGGGACGTTGTAGGTCTACCTCCTGG			
3' OH 5' P			
GGTAGTTGCCGAAGGTGC		AM1 Ir1	
GGTAGTTGCCGAAGGTGC			
TTCAAGGAGAACTACCGCTTCCAG			
CCATCAACGGCTACATCATGGACACCTGCCCGCCCTGGTGTATGGCCCCAGGACCGCATCCGCTGGTACCCCTACAA			
AAGTTCCTCTTGATGGCGAAGGTGC			
GGTAGTTGCCGAAGGTGC			
CCGAGTTCCTTGTAGTACCTGTGGGACGGGCCGGAACCACTACCGGGTCTCTGGTCCGCTAGGCGACCATGGGATGTT			

GCTTTAC
CGAAATG

FIG. 51

Fragment J

<p>EcoRI BstEII</p> <p>GTAGAA¹TCGTAGGGT²GACCTTCCGCAACCAAGCCAGCCGCCCTTACAGCTTCTACAGCAGCCTGATCAGGTACGAGGAGCACAGCGCC</p> <p>CATCTTAAGCATCCCACTGGAAGCGTTGGTCCGGTCGGCGGGGATGTCGAAGATGTGTCGGACTAGTCGATGCTCCTCTGGTCCGG</p>	<p>AM1 Jf1</p>
<p>AGG³CGCGGAGCCCGCAAGAACTTC⁴ GTGAAGCCCAACGAGACCAAGACCTACTTCTGGAAGGTGCAGCACCATGGCCCCCACCAA</p> <p>TCC⁵ CGCGGCTCGGGGCGTTCTTTGAAG⁶CACTTCGGGTGCTCTGGTTCTGGATGAAGACCTTCCACGTCGTGGTGTACCGGGGGTGGTT</p> <p>5' P 3' OH</p>	<p>AM1 Jr3</p>
<p>GGACGAGTTTCGACTGCAAGGCCTGGGCCTACTTTCAG⁷CGACGTGGACCTGGAGAAGGAC⁸ GTGCACAGCGGCCTGATCGGCCCTGCTG</p> <p>CCTGCTCAAGCTGACGTTCCGGACCCCGGATGAAGTC⁹ GCTGCACCTGGACCTCTTCCCTG¹⁰CACGTGTCCCGGACTAGCCCGGGGACGAC</p> <p>5' P 3' OH</p>	<p>AM1 Jr2</p>
<p>AM1 Jf3 EagI BstEII HindIII</p> <p>GTGTGCCACACCAACACCCCTGAACCCCGCCACGCGCGCCAGGTGACCCCTACAAAGCTTTTAC</p> <p>CACACGGTGTGGTGTGGGACTTGGGGCGGGTGC CGCGGCTCCACTGGGATGTTCCGAAATG</p>	<p>AM1 Jr1</p>

FIG. 5J

Fragment K

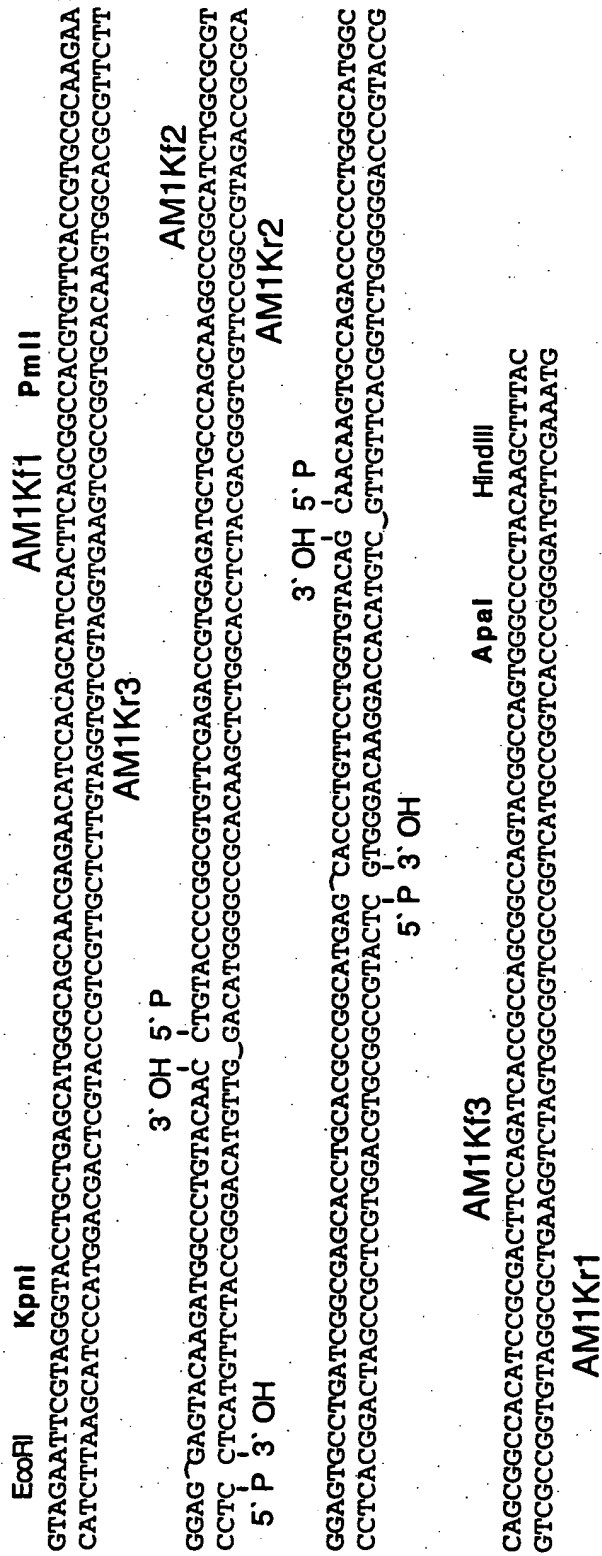


FIG. 5K

Fragment L

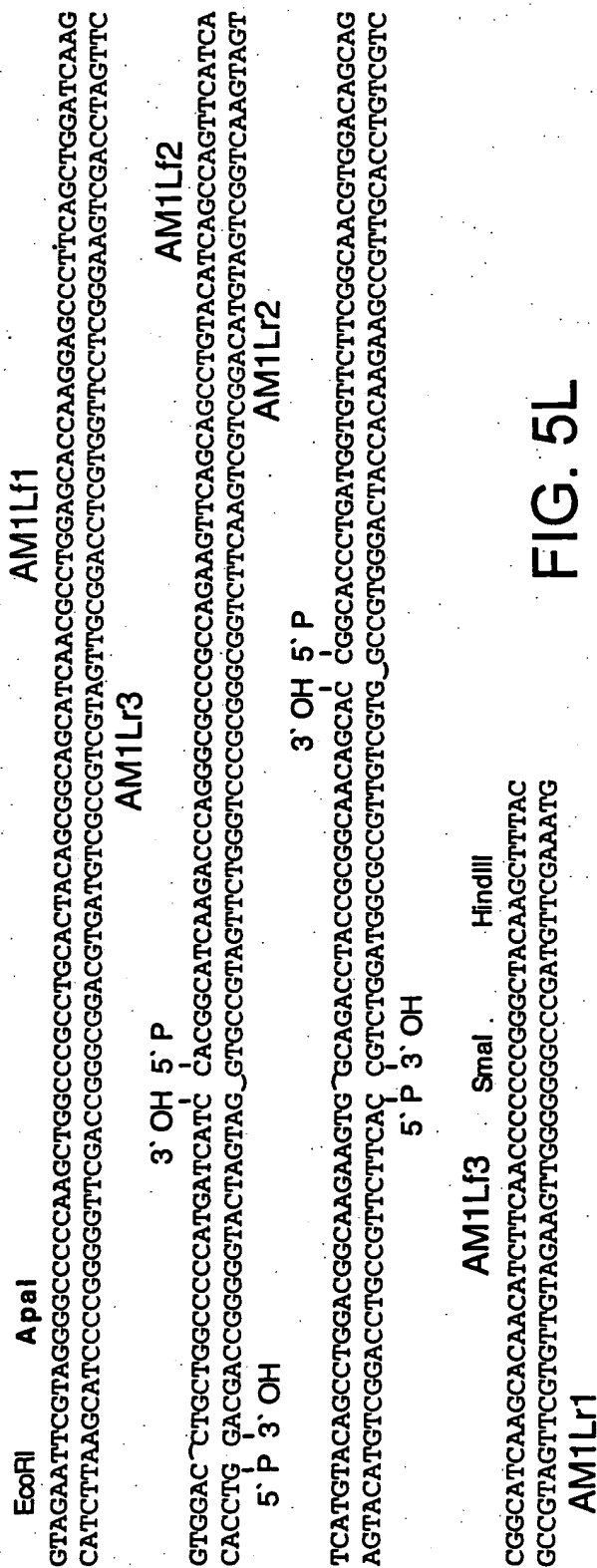


FIG. 5L

Fragment M

EcoRI	EcoRV	AM1Mf1
GTAGAATTCCGTAGGATATCATCGCCCGCTACATCCGCCTGCACCCCACTACAGCATCCGAGCACCCCTGCGCATGGAGCTGATGGG		
CATCTTAAGCATCCTATAGTAGCGGGCGATGTAGGCGGACGTGGGGTGGTGATGTCGTAGGCGTCTGTGGACGCGTACCTCGACTACCC		
		AM1Mf2
CTGCGACCTTGAACAGCTGCAGCATGCCCTTGG	GCATGGAGAGCAAGGCCATCAGCGACGCCCCAGATCACCGCCAGCAGCTACTTCACC	
GACGCTG	GACTTGTGACGTCGTACGGGGACC	CGTACCCTCTCGTTCCGGTAGTCGCTGCGGGTCTAGTGGCGGTCGTCGATGAAGTGG
5' P	3' OH	AM1Mr2
AACATGTTCCGCCACCTGGAGCCCAAGGCC	CGCCTGCACCTGCAGGGCCGCAG	CAACGCCCTGGCGCCCCCAGGTGAACAACCCCA
TTGTACAAGCGGTGGACCTCGGGTTCGTTCCGG	GCGGACGTGGACGTCCTCCGGCGTC	GTTGCGGACCCCGGGGTCCACTTGTGGGGT
5' P	3' OH	
AM1Mf3	BstEII	HindIII
AGGAGTGGCTGCAGGTGGACTTCAGAAAGACCAATGAAGGTGACCCCTACAAGCTTTAC		
TCCTCACCGACGTCCACCTGAAGGTCTTCTGGTACTTCCACTGGGATGTTCGAAATG		
		AM1Mr1

FIG. 5M

FIG. 5N

HindIII
CAAGCTTAC
GTTCGAAATG

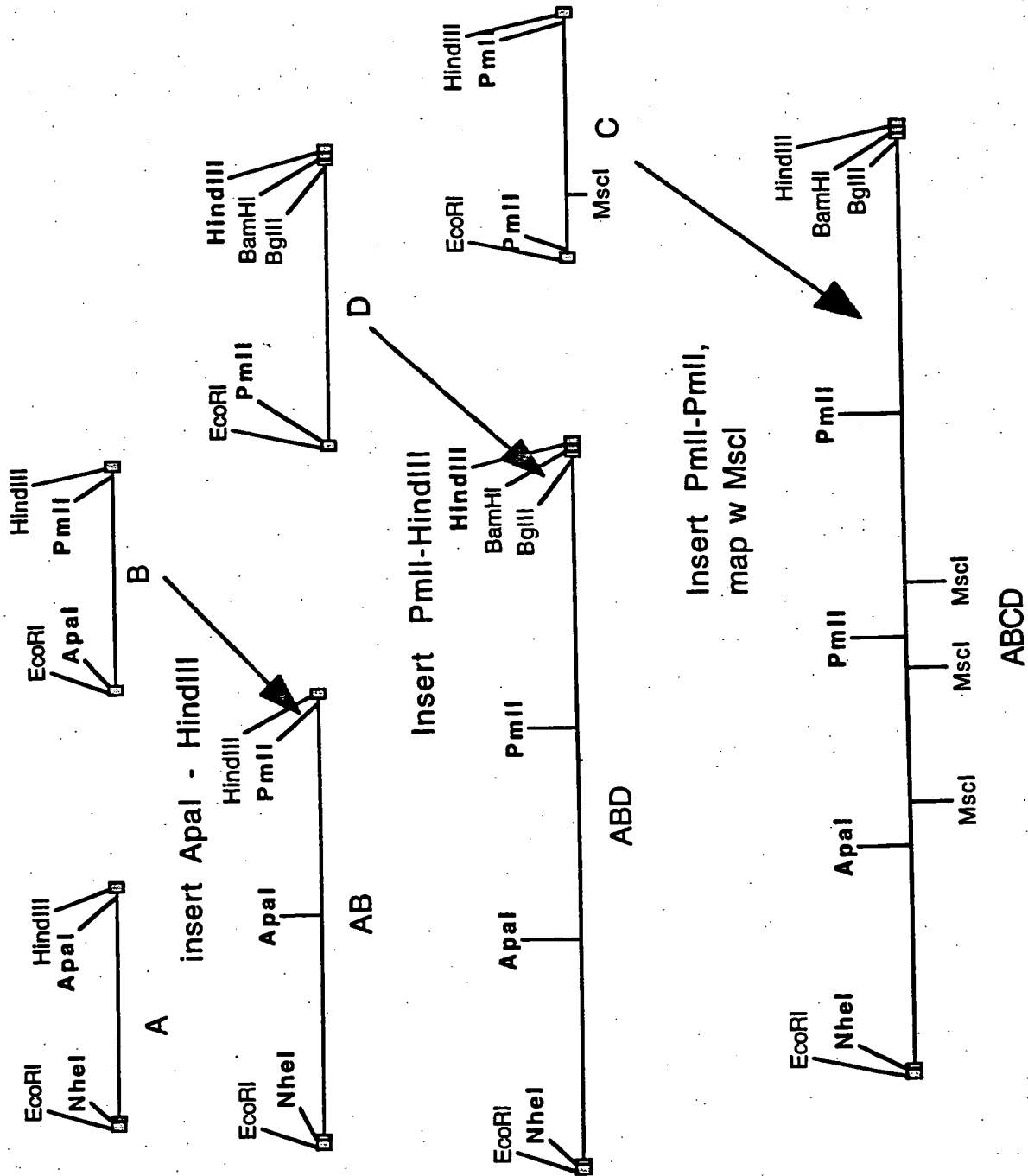


FIG. 6A

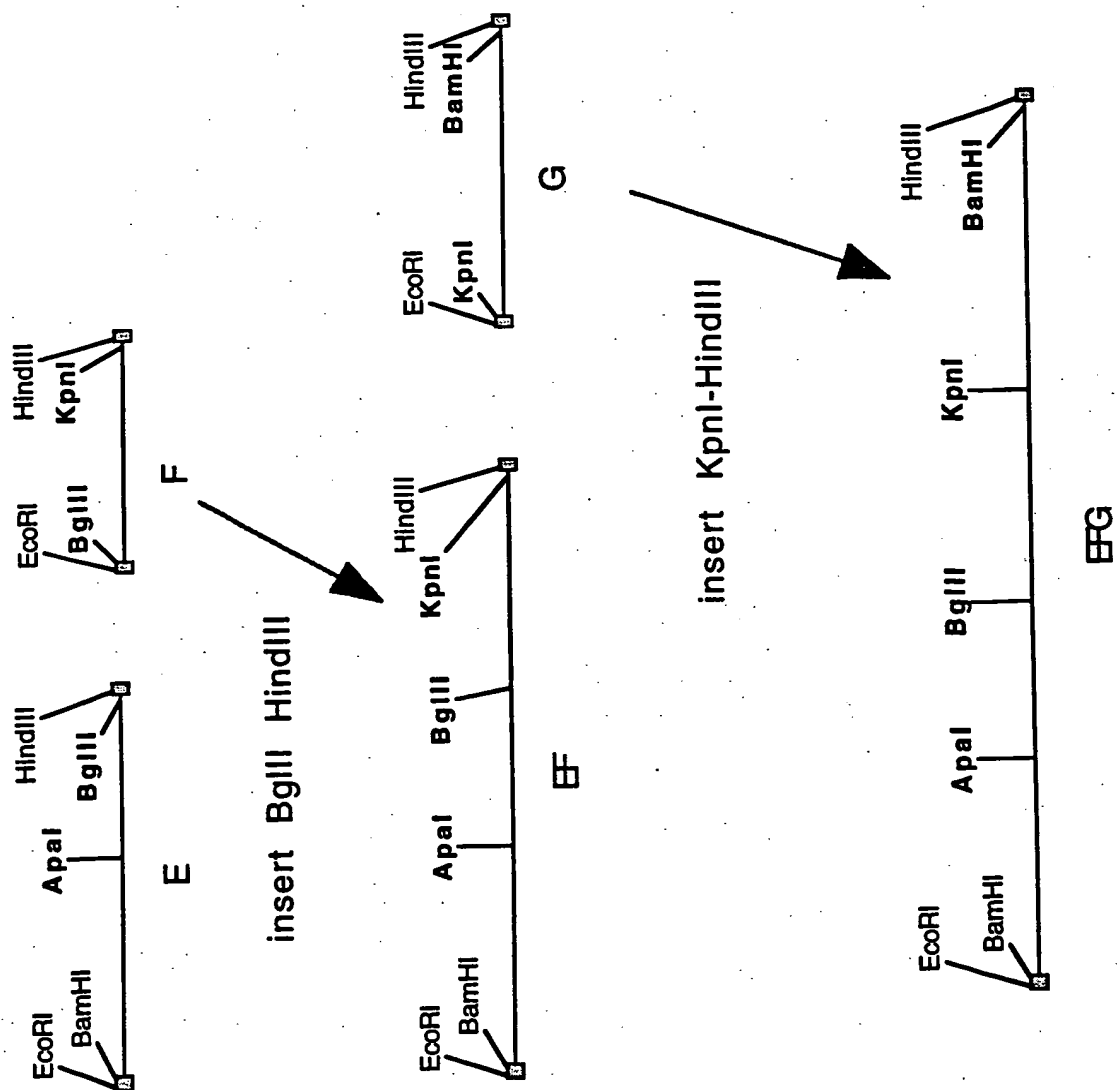


FIG. 6B

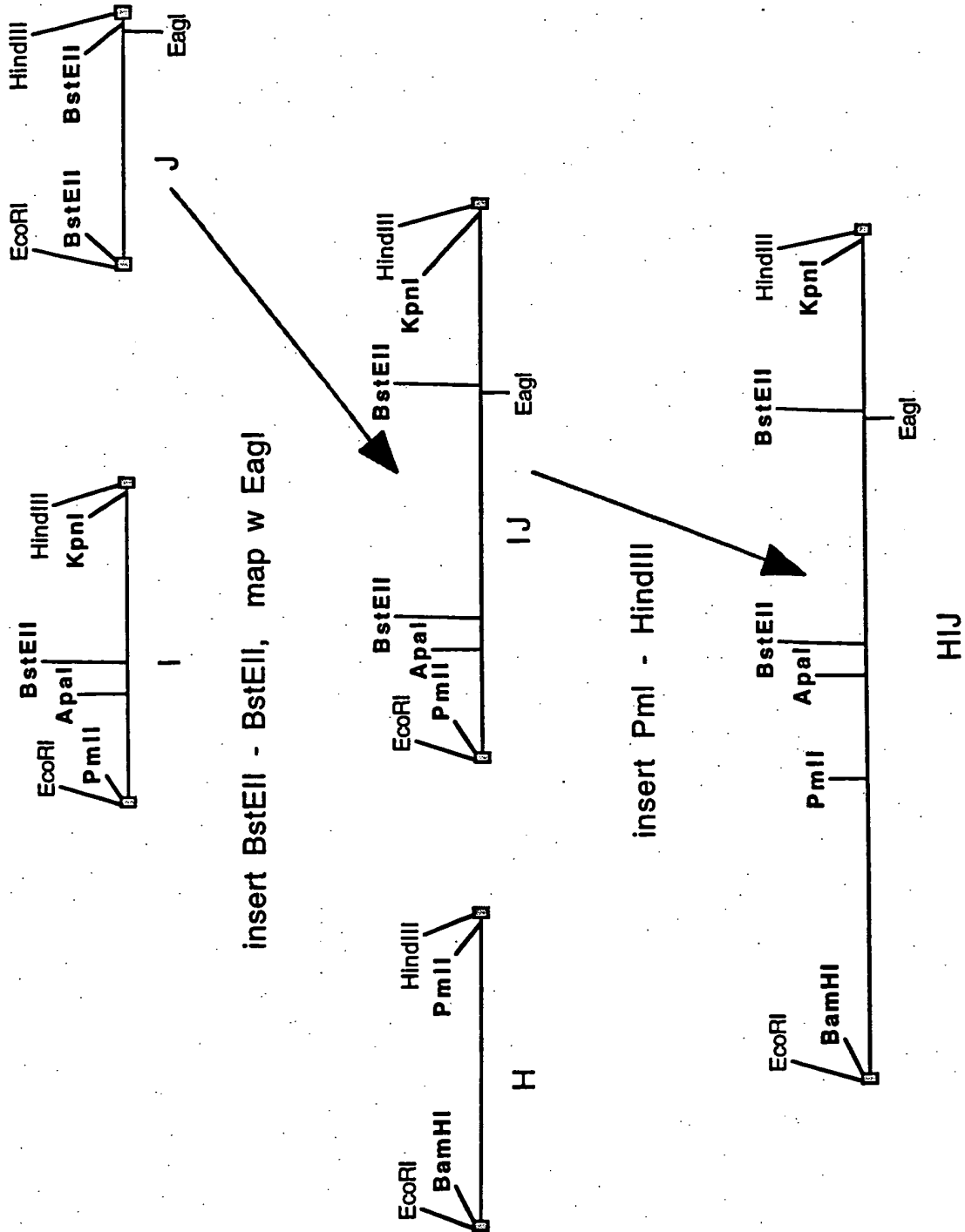


FIG. 6C

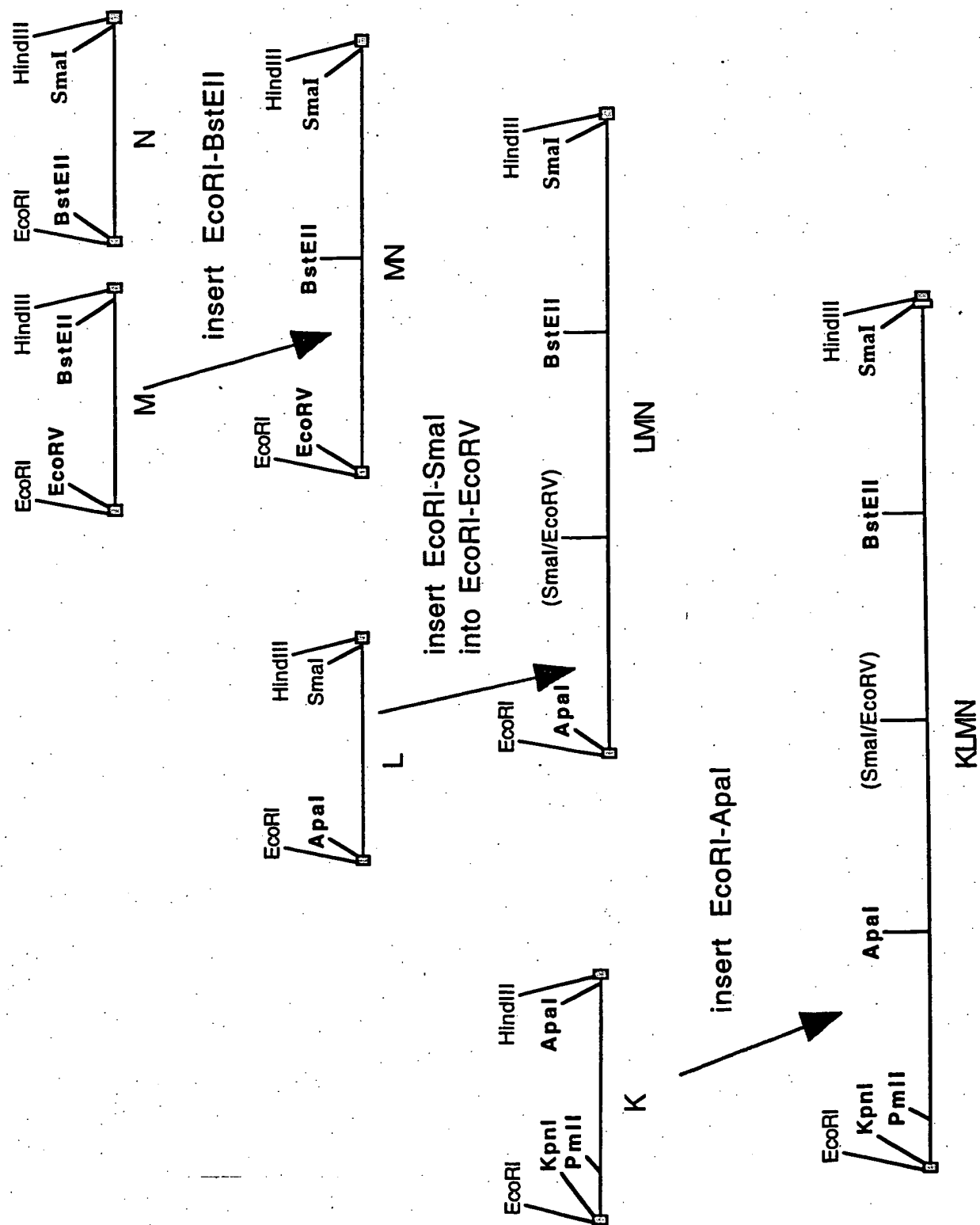
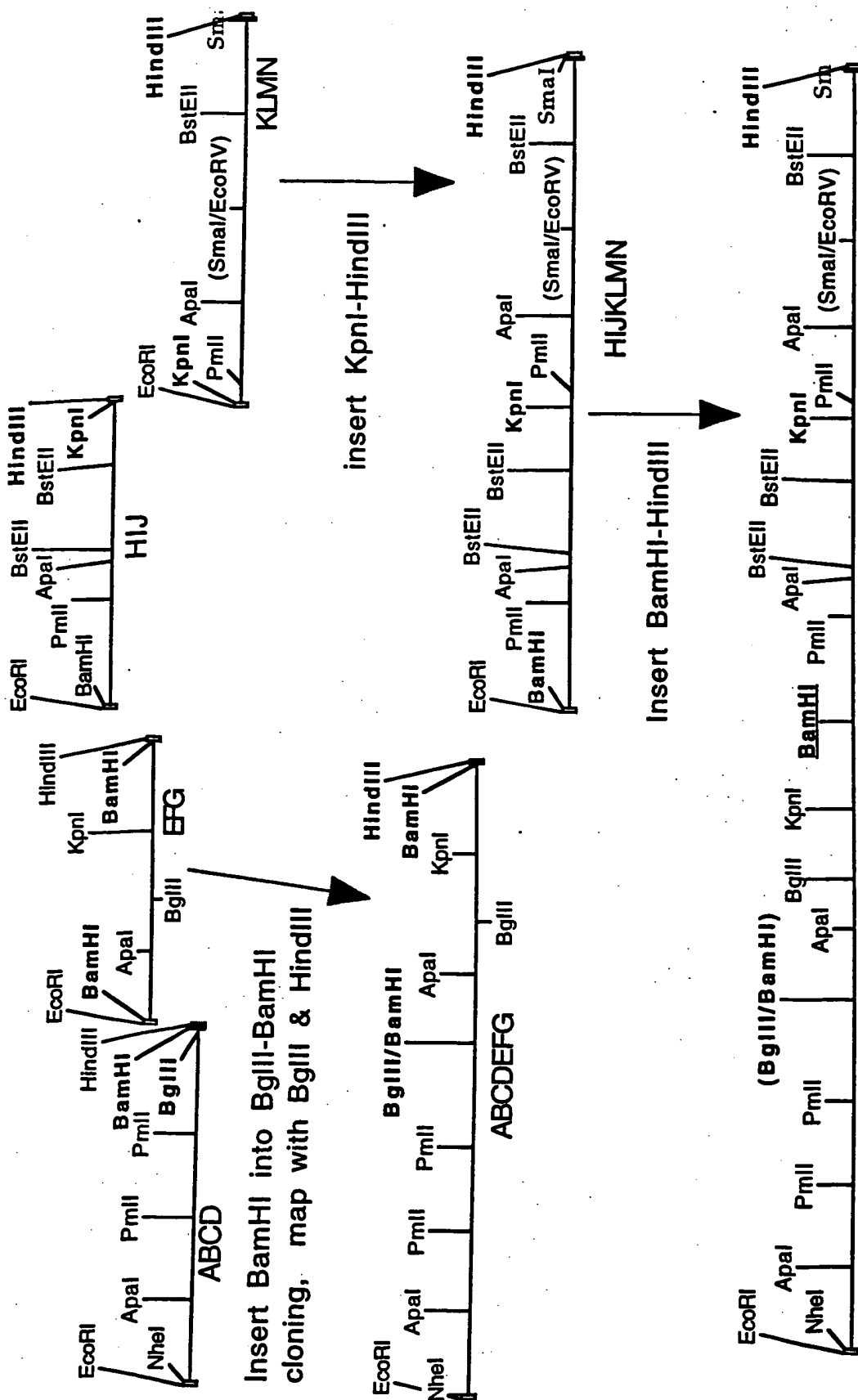


FIG. 6D



ABCDEFGHIJKLMNOP, i.e. pAM1-1

FIG. 6E

EcoRI NheI

1 TAGAATTCGTAGGCTAGCATGCAGATCGAGCTGAGCACCTGCTTCTTCCTGTGCCTGCTGCGCTTCTGCTTC
1 MetGlnIleGluLeuSerThrCysPhePheLeuCysLeuLeuArgPheCysPhe

73 AGCGCCACCCGCCGCTACTACCTGGGCGCCGTGGAGCTGAGCTGGGACTACATGCAGAGCGACCTGGGCGAG
19 SerAlaThrArgArgTyrTyrLeuGlyAlaValGluLeuSerTrpAspTyrMetGlnSerAspLeuGlyGlu

145 CTGCCCCGTGGACGCCCGCTTCCCCCCCCGCGTGCCCAAGAGCTTCCCCTTCAACACCAGCGTGGTGTACAAG
43 LeuProValAspAlaArgPheProProArgValProLysSerPheProPheAsnThrSerValValTyrLys

217 AAGACCCTGTTCGTGGAGTTACCGACCACCTGTTCAACATCGCCAAGCCCCGCCCCCCTGGATGGGCCTG
67 LysThrLeuPheValGluPheThrAspHisLeuPheAsnIleAlaLysProArgProProTrpMetGlyLeu

Apal MscI

289 CTGGGCCCCACCATCCAGGCCGAGGTGTACGACACCGTGGTGATCACCCTGAAGAATATGGCCAGCCACCCC
91 LeuGlyProThrIleGlnAlaGluValTyrAspThrValValIleThrLeuLysAsnMetAlaSerHisPro

361 GTGAGCCTGCACGCCGTGGGCGTGAGCTACTGGAAGGCCAGCGAGGGCGCCGAGTACGACGACCAGACCAGC
115 ValSerLeuHisAlaValGlyValSerTyrTrpLysAlaSerGluGlyAlaGluTyrAspAspGlnThrSer

433 CAGCGCGAGAAGGAGGACGACAAGGTGTTCCCCGGCGGCAGCCACACCTACGTGTGGCAGGTGCTGAAGGAG
139 GlnArgGluLysGluAspAspLysValPheProGlyGlySerHisThrTyrValTrpGlnValLeuLysGlu

MscI PmlI

505 AACGGCCCCATGGCCAGCGACCCCTGTGCCTGACCTACAGCTACCTGAGCCACGTGGACCTGGTGAAGGAC
163 AsnGlyProMetAlaSerAspProLeuCysLeuThrTyrSerTyrLeuSerHisValAspLeuValLysAsp

MscI

577 CTGAACAGCGGCCTGATCGGCGCCCTGCTGGTGTGCCGCGAGGGCAGCCTGGCCAAGGAGAAGACCCAGACC
187 LeuAsnSerGlyLeuIleGlyAlaLeuLeuValCysArgGluGlySerLeuAlaLysGluLysThrGlnThr

649 CTGCACAAGTTCATCCTGCTGTTTCGCCGTGTTTCGACGAGGGCAAGAGCTGGCACAGCGAGACCAAGAACAGC
211 LeuHisLysPheIleLeuLeuPheAlaValPheAspGluGlyLysSerTrpHisSerGluThrLysAsnSer

721 CTGATGCAGGACCGCGACGCCCGCCAGCGCCCCGCGCCTGGCCCAAGATGCACACCGTGAACGGCTACGTGAAC
235 LeuMetGlnAspArgAspAlaAlaSerAlaArgAlaTrpProLysMetHisThrValAsnGlyTyrValAsn

PmlI

793 CGCAGCCTGCCCCGGCCTGATCGGCTGCCACCGCAAGAGCGTGTACTGGCACGTGATCGGCATGGGCAACCACC
259 ArgSerLeuProGlyLeuIleGlyCysHisArgLysSerValTyrTrpHisValIleGlyMetGlyThrThr

865 CCCGAGGTGCACAGCATCTTCCTGGAGGGCCACACCTTCCTGGTGCGCAACCACCGCCAGGCCAGCCTGGAG
283 ProGluValHisSerIlePheLeuGluGlyHisThrPheLeuValArgAsnHisArgGlnAlaSerLeuGlu

937 ATCAGCCCCATCACCTTCCTGACCGCCAGACCCTGCTGATGGACCTGGGCCAGTTTCCTGCTGTTCTGCCAC
307 IleSerProIleThrPheLeuThrAlaGlnThrLeuLeuMetAspLeuGlyGlnPheLeuLeuPheCysHis

1009 ATCAGCAGCCACCAGCACGACGGCATGGAGGCCTACGTGAAGGTGGACAGCTGCCCCGAGGAGCCCCAGCTG
331 IleSerSerHisGlnHisAspGlyMetGluAlaTyrValLysValAspSerCysProGluGluProGlnLeu

1081 CGCATGAAGAACAACGAGGAGGCCGAGGACTACGACGACGACCTGACCGACAGCGAGATGGACGTGGTGCGC
355 ArgMetLysAsnAsnGluGluAlaGluAspTyrAspAspLeuThrAspSerGluMetAspValValArg

(BglII/BamHI)

1153 TTCGACGACGACAACAGCCCCAGCTTCATCCAGATCCGCAGCGTGGCCAAGAAGCACCCCAAGACCTGGGTG
379 PheAspAspAspAsnSerProSerPheIleGlnIleArgSerValAlaLysLysHisProLysThrTrpVal

1225 CACTACATCGCCGCGGAGGAGGAGGACTGGGACTACGCCCCCTGGTGCTGGCCCCCGACGACCGCAGCTAC
403 HisTyrIleAlaAlaGluGluGluAspTrpAspTyrAlaProLeuValLeuAlaProAspAspArgSerTyr

EagI

1297 AAGAGCCAGTACCTGAACAACGGCCCCCAGCGCATCGGCCGCAAGTACAAGAAGGTGCGCTTCATGGCCTAC
427 LysSerGlnTyrLeuAsnAsnGlyProGlnArgIleGlyArgLysTyrLysLysValArgPheMetAlaTyr

Apal

1369 ACCGACGAGACCTTCAAGACCCGCGAGGCCATCCAGCACGAGAGCGGCATCCTGGGCCCCCTGCTGTACGGC
451 ThrAspGluThrPheLysThrArgGluAlaIleGlnHisGluSerGlyIleLeuGlyProLeuLeuTyrGly

FIG. 7A

1441 GAGGTGGGCGACACCCTGCTGATCATCTTCAAGAACCAGGCCAGCCGCCCTACAACATCTACCCCCACGGC
475▶ GluValGlyAspThrLeuLeuIleIlePheLysAsnGlnAlaSerArgProTyrAsnIleTyrProHisGly
1513 ATCACCAGCGTGCAGCCCCCTGTACAGCCGCCGCTGCCCAAGGGCGTGAAGCACCTGAAGGACTTCCCCATC
499▶ IleThrAspValArgProLeuTyrSerArgArgLeuProLysGlyValLysHisLeuLysAspPheProIle

BglII

1585 CTGCCCCGGCGAGATCTTCAAGTACAAGTGGACCGTGACCGTGGAGGACGGCCCCACCAAGAGCGACCCCCGC
523▶ LeuProGlyGluIlePheLysTyrLysTrpThrValThrValGluAspGlyProThrLysSerAspProArg
1657 TGCCTGACCCGCTACTACAGCAGCTTCGTGAACATGGAGCGCGACCTGGCCAGCGGCCTGATCGGCCCCCTG
547▶ CysLeuThrArgTyrTyrSerSerPheValAsnMetGluArgAspLeuAlaSerGlyLeuIleGlyProLeu
1729 CTGATCTGCTACAAGGAGAGCGTGGACCAGCGCGGCAACCAGATCATGAGCGACAAGCGCAACGTGATCCTG
571▶ LeuIleCysTyrLysGluSerValAspGlnArgGlyAsnGlnIleMetSerAspLysArgAsnValIleLeu

KpnI

1801 TTCAGCGTGTTCGACGAGAACCAGCAGCTGGTACCTGACCGAGAACATCCAGCGCTTCCTGCCCAACCCCCGC
595▶ PheSerValPheAspGluAsnArgSerTrpTyrLeuThrGluAsnIleGlnArgPheLeuProAsnProAla
1873 GCGGTGCAGCTGGAGGACCCCCGAGTTCAGGCCAGCAACATCATGCACAGCATCAACGGCTACGTGTTTCGAC
619▶ GlyValGlnLeuGluAspProGluPheGlnAlaSerAsnIleMetHisSerIleAsnGlyTyrValPheAsp
1945 AGCCTGCAGCTGAGCGTGTGCCTGCACGAGGTGGCCTACTGGTACATCCTGAGCATCGGCGCCCAGACCGAC
643▶ SerLeuGlnLeuSerValCysLeuHisGluValAlaTyrTrpTyrIleLeuSerIleGlyAlaGlnThrAsp
2017 TTCCTGAGCGTGTTCCTCAGCGGCTACACCTTCAAGCACAAAGATGGTGTACGAGGACACCTGACCTGTTC
667▶ PheLeuSerValPhePheSerGlyTyrThrPheLysHisLysMetValTyrGluAspThrLeuThrLeuPhe

BamHI

2089 CCCTTCAGCGGCGAGACCGTGTTCATGAGCATGGAGAACCCCGGCCTGTGGATCCTGGGCTGCCACAACAGC
691▶ ProPheSerGlyGluThrValPheMetSerMetGluAsnProGlyLeuTrpIleLeuGlyCysHisAsnSer
2161 GACTTCCGCAACCGCGGCATGACCGCCCTGCTGAAGGTGAGCAGCTGCGACAAGAACACCGGCGACTACTAC
715▶ AspPheArgAsnArgGlyMetThrAlaLeuLeuLysValSerSerCysAspLysAsnThrGlyAspTyrTyr
2233 GAGGACAGCTACGAGGACATCAGCGCCTACCTGCTGAGCAAGAACAACGCCATCGAGCCCCGCCTGGAGGAG
739▶ GluAspSerTyrGluAspIleSerAlaTyrLeuLeuSerLysAsnAsnAlaIleGluProArgLeuGluGlu

BstXI

2305 ATCACCCGCACACCCTGCAGAGCGACCAGGAGGAGATCGACTACGACGACACCATCAGCGTGGAGATGAAG
763▶ IleThrArgThrThrLeuGlnSerAspGlnGluGluIleAspTyrAspAspThrIleSerValGluMetLys
2377 AAGGAGGACTTCGACATCTACGACGAGGACGAGAACCAGAGCCCCCGAGCTTCCAGAAGAAGACCCGCCAC
787▶ LysGluAspPheAspIleTyrAspGluAspGluAsnGlnSerProArgSerPheGlnLysLysThrArgHis

PmlI

2449 TACTTCATCGCCGCCGTGGAGCGCCTGTGGGACTACGGCATGAGCAGCAGCCCCCACGTGCTGCGCAACCGC
811▶ TyrPheIleAlaAlaValGluArgLeuTrpAspTyrGlyMetSerSerSerProHisValLeuArgAsnArg
2521 GCCCAGAGCGGCAGCGTGCCTCAGTTCAAGAAGGTGGTGTCCAGGAGTTCACCGACGGCAGCTTACCCAG
835▶ AlaGlnSerGlySerValProGlnPheLysLysValValPheGlnGluPheThrAspGlySerPheThrGln

Apal

2593 CCCCTGTACCGCGCGAGCTGAACGAGCACCTGGGCCTGCTGGGCCCCCTACATCCGCGCCGAGGTGGAGGAC
859▶ ProLeuTyrArgGlyGluLeuAsnGluHisLeuGlyLeuLeuGlyProTyrIleArgAlaGluValGluAsp

BstEII

2665 AACATCATGGTGACCTTCCGCAACCAGGCCAGCCGCCCTACAGCTTCTACAGCAGCCTGATCAGCTACGAG
883▶ AsnIleMetValThrPheArgAsnGlnAlaSerArgProTyrSerPheTyrSerSerLeuIleSerTyrGlu
2737 GAGGACCAGCGCCAGGGCGCCGAGCCCCGCAAGAACTTCGTGAAGCCCAACGAGACCAAGACCTACTTCTGG
907▶ GluAspGlnArgGlnGlyAlaGluProArgLysAsnPheValLysProAsnGluThrLysThrTyrPheTrp
2809 AAGGTGCAGCACCATGGCCCCACCAAGGACGAGTTCGACTGCAAGGCCTGGGCCTACTTCAGCGACGTG
931▶ LysValGlnHisHisMetAlaProThrLysAspGluPheAspCysLysAlaTrpAlaTyrPheSerAspVal

FIG. 7B

2881 GACCTGGAGAAGGACGTGCACAGCGGCCTGATCGGCCCCCTGCTGGTGTGCCACACCAACACCCTGAACCCC
955▴ AspLeuGluLysAspValHisSerGlyLeuIleGlyProLeuLeuValCysHisThrAsnThrLeuAsnPro
EagI BstEII
2953 GCCCACGGCCGCCAGGTGACCGTGCAGGAGTTCGCCCTGTCTTCACCATCTTCGACGAGACCAAGAGCTGG
979▴ AlaHisGlyArgGlnValThrValGlnGluPheAlaLeuPhePheThrIlePheAspGluThrLysSerTrp
3025 TACTTCACCGAGAACATGGAGCGCAACTGCCGCGCCCCCTGCAACATCCAGATGGAGGACCCCACTTCAAG
1003▴ TyrPheThrGluAsnMetGluArgAsnCysArgAlaProCysAsnIleGlnMetGluAspProThrPheLys
3097 GAGAACTACCGCTTCCACGCCATCAACGGCTACATCATGGACACCCTGCCCGGCCCTGGTGTATGGCCCAGGAC
1027▴ GluAsnTyrArgPheHisAlaIleAsnGlyTyrIleMetAspThrLeuProGlyLeuValMetAlaGlnAsp
KpnI PmlI
3169 CAGCGCATCCGCTGGTACCTGCTGAGCATGGGCAGCAACGAGAACATCCACAGCATCCACTTCAGCGGCCAC
1051▴ GlnArgIleArgTrpTyrLeuLeuSerMetGlySerAsnGluAsnIleHisSerIleHisPheSerGlyHis
3241 GTGTTACCGTGCGCAAGAAGGAGGAGTACAAGATGGCCCCGTGACAACCTGTACCCCGGCGTGTTCGAGACC
1075▴ ValPheThrValArgLysLysGluGluTyrLysMetAlaLeuTyrAsnLeuTyrProGlyValPheGluThr
3313 GTGGAGATGCTGCCCAGCAAGGCCGGCATCTGGCGCGTGGAGTGCCTGATCGGCGAGCACCTGCACGCCGGC
1099▴ ValGluMetLeuProSerLysAlaGlyIleTrpArgValGluCysLeuIleGlyGluHisLeuHisAlaGly
3385 ATGAGCACCCCTGTTTCCTGGTGTACAGCAACAAGTGCCAGACCCCCCTGGGCATGGCCAGCGGCCACATCCGC
1123▴ MetSerThrLeuPheLeuValTyrSerAsnLysCysGlnThrProLeuGlyMetAlaSerGlyHisIleArg
ApaI
3457 GACTTCCAGATCACCGCCAGCGGCCAGTACGGCCAGTGGGCCCCCAAGCTGGCCCGCCTGCACTACAGCGGC
1147▴ AspPheGlnIleThrAlaSerGlyGlnTyrGlyGlnTrpAlaProLysLeuAlaArgLeuHisTyrSerGly
3529 AGCATCAACGCCTGGAGCACCAAGGAGCCCTTCAGCTGGATCAAGGTGGACCTGCTGGCCCCCATGATCATC
1171▴ SerIleAsnAlaTrpSerThrLysGluProPheSerTrpIleLysValAspLeuLeuAlaProMetIleIle
3601 CACGGCATCAAGACCCAGGGCGCCCGCCAGAAAGTTCAGCAGCCTGTACATCAGCCAGTTCATCATCATGTAC
1195▴ HisGlyIleLysThrGlnGlyAlaArgGlnLysPheSerSerLeuTyrIleSerGlnPheIleIleMetTyr
3673 AGCCTGGACGGCAAGAAGTGGCAGACCTACCGCGGCAACAGCACCGGCACCCTGATGGTGTCTTCGGCAAC
1219▴ SerLeuAspGlyLysLysTrpGlnThrTyrArgGlyAsnSerThrGlyThrLeuMetValPhePheGlyAsn
(SmaI/EcoRV)
3745 GTGGACAGCAGCGGCATCAAGCACAACATCTTCAACCCCCCATCATCGCCCGCTACATCCGCCTGCACCCC
1243▴ ValAspSerSerGlyIleLysHisAsnIlePheAsnProProIleIleAlaArgTyrIleArgLeuHisPro
3817 ACCCACTACAGCATCCGCAGCACCCCTGCGCATGGAGCTGATGGGCTGCGACCTGAACAGCTGCAGCATGCCC
1267▴ ThrHisTyrSerIleArgSerThrLeuArgMetGluLeuMetGlyCysAspLeuAsnSerCysSerMetPro
3889 CTGGGCATGGAGAGCAAGGCCATCAGCGACGCCCAGATCACCGCCAGCAGCTACTTACCAACATGTTTCGCC
1291▴ LeuGlyMetGluSerLysAlaIleSerAspAlaGlnIleThrAlaSerSerTyrPheThrAsnMetPheAla
3961 ACCTGGAGCCCCAGCAAGGCCCGCCTGCACCTGCAGGGCCGAGCAACGCCTGGCGCCCCCAGGTGAACAAC
1315▴ ThrTrpSerProSerLysAlaArgLeuHisLeuGlnGlyArgSerAsnAlaTrpArgProGlnValAsnAsn
BstEII
4033 CCCAAGGAGTGGCTGCAGGTGGACTTCCAGAAGACCATGAAGGTGACCGGCGTGACCACCCAGGGCGTGAAG
1339▴ ProLysGluTrpLeuGlnValAspPheGlnLysThrMetLysValThrGlyValThrThrGlnGlyValLys
4105 AGCCTGCTGACCAGCATGTACGTGAAGGAGTTCCTGATCAGCAGCAGCCAGGACGGCCACCACTGGACCCTG
1363▴ SerLeuLeuThrSerMetTyrValLysGluPheLeuIleSerSerSerGlnAspGlyHisGlnTrpThrLeu
4177 TTCTTCCAGAACGGCAAGGTGAAGGTGTTCCAGGGCAACCAGGACAGCTTACCCCCGTGGTGAACAGCCTG
1387▴ PhePheGlnAsnGlyLysValLysValPheGlnGlyAsnGlnAspSerPheThrProValValAsnSerLeu
4249 GACCCCCCCTGCTGACCCGCTACCTGCGCATCCACCCCCAGAGCTGGGTGCACCAGATCGCCCTGCGCATG
1411▴ AspProProLeuLeuThrArgTyrLeuArgIleHisProGlnSerTrpValHisGlnIleAlaLeuArgMet
SmaI HindIII
4321 GAGGTGCTGGGCTGCGAGGCCAGGACCTGTACTAGCTGCCCGGGCTACAAGCTTT
1435▴ GluValLeuGlyCysGluAlaGlnAspLeuTyr...

FIG. 7C

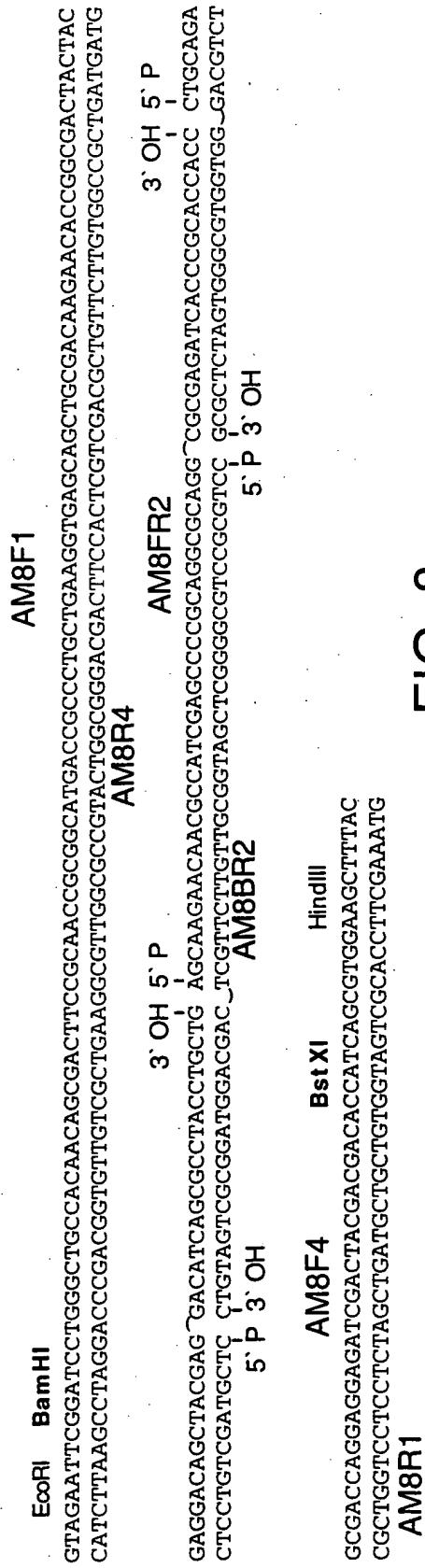


FIG. 8

EcoRI NheI

1 TAGAATTCGTAGGCTAGCATGCAGATCGAGCTGAGCACCTGCTTCTTCTGTGCCTGTCTGCGCTTCTGCTTC
1▶ MetGlnIleGluLeuSerThrCysPhePheLeuCysLeuLeuArgPheCysPhe

73 AGCGCCACCCGCCGCTACTACCTGGGCGCCGTGGAGCTGAGCTGGGACTACATGCAGAGCGACCTGGGCGAG
19▶ SerAlaThrArgArgTyrTyrLeuGlyAlaValGluLeuSerTrpAspTyrMetGlnSerAspLeuGlyGlu

145 CTGCCCCGTGGACGCCCGCTTCCCCCCCCGCGTGCCCAAGAGCTTCCCCCTCAACACCAGCGTGGTGTACAAG
43▶ LeuProValAspAlaArgPheProProArgValProLysSerPheProPheAsnThrSerValValTyrLys

217 AAGACCCTGTTCGTGGAGTTCACCGACCACCTGTTCAACATCGCCAAGCCCCGCCCCCTGGATGGGCCTG
67▶ LysThrLeuPheValGluPheThrAspHisLeuPheAsnIleAlaLysProArgProProTrpMetGlyLeu

Apal MscI

289 CTGGGCCCCACCATCCAGGCCGAGGTGTACGACACCGTGGTGATCACCTGAAGAACATGGCCAGCCACCCC
91▶ LeuGlyProThrIleGlnAlaGluValTyrAspThrValValIleThrLeuLysAsnMetAlaSerHisPro

361 GTGAGCCTGCACGCCGTGGGCGTGAGCTACTGGAAGGCCAGCGAGGGCGCCGAGTACGACGACCAGACCAGC
115▶ ValSerLeuHisAlaValGlyValSerTyrTrpLysAlaSerGluGlyAlaGluTyrAspAspGlnThrSer

433 CAGCGCGAGAAGGAGGACGACAAGGTGTTCCCCGGCGGCAGCCACACCTACGTGTGGCAGGTGCTGAAGGAG
139▶ GlnArgGluLysGluAspAspLysValPheProGlyGlySerHisThrTyrValTrpGlnValLeuLysGlu

MscI PmlI

505 AACGGCCCCATGGCCAGCGACCCCCTGTGCCTGACCTACAGCTACCTGAGCCACGTGGACCTGGTGAAGGAC
163▶ AsnGlyProMetAlaSerAspProLeuCysLeuThrTyrSerTyrLeuSerHisValAspLeuValLysAsp

MscI

577 CTGAACAGCGGCCTGATCGGCGCCCTGCTGGTGTGCCGCGAGGGCAGCCTGGCCAAGGAGAAGACCCAGACC
187▶ LeuAsnSerGlyLeuIleGlyAlaLeuLeuValCysArgGluGlySerLeuAlaLysGluLysThrGlnThr

649 CTGCACAAGTTCATCCTGCTGTTGCGCGTGTTCGACGAGGGCAAGAGCTGGCACAGCGAGACCAAGAACAGC
211▶ LeuHisLysPheIleLeuLeuPheAlaValPheAspGluGlyLysSerTrpHisSerGluThrLysAsnSer

721 CTGATGCAGGACCGCGACGCCGCCAGCGCCCGCGCCTGGCCCAAGATGCACACCGTGAACGGCTACGTGAAC
235▶ LeuMetGlnAspArgAspAlaAlaSerAlaArgAlaTrpProLysMetHisThrValAsnGlyTyrValAsn

PmlI

793 CGCAGCCTGCCCCGGCCTGATCGGCTGCCACCGCAAGAGCGTGTACTGGCACGTGATCGGCATGGGCACCACC
259▶ ArgSerLeuProGlyLeuIleGlyCysHisArgLysSerValTyrTrpHisValIleGlyMetGlyThrThr

865 CCCGAGGTGCACAGCATCTTCTTGGAGGGCCACACCTTCTTGGTGCGCAACCACCGCCAGGCCAGCCTGGAG
283▶ ProGluValHisSerIlePheLeuGluGlyHisThrPheLeuValArgAsnHisArgGlnAlaSerLeuGlu

937 ATCAGCCCCATCACCTTCTTGACCGCCAGACCCTGCTGATGGACCTGGGCCAGTTCTCTGCTGTTCTGCCAC
307▶ IleSerProIleThrPheLeuThrAlaGlnThrLeuLeuMetAspLeuGlyGlnPheLeuLeuPheCysHis

1009 ATCAGCAGCCACCAGCAGCAGCGGCATGGAGGCCTACGTGAAGGTGGACAGCTGCCCCGAGGAGCCCCAGCTG
331▶ IleSerSerHisGlnHisAspGlyMetGluAlaTyrValLysValAspSerCysProGluGluProGlnLeu

1081 CGCATGAAGAACAACGAGGAGGCCGAGGACTACGACGACGACCTGACCGACAGCGAGATGGACGTGGTGC GC
355▶ ArgMetLysAsnAsnGluGluAlaGluAspTyrAspAspAspLeuThrAspSerGluMetAspValValArg

(BglII/BamHI)

1153 TTCGACGACGACAACAGCCCCAGCTTCATCCAGATCCGCAGCGTGGCCAAGAAGCACCCCAAGACCTGGGTG
379▶ PheAspAspAspAsnSerProSerPheIleGlnIleArgSerValAlaLysLysHisProLysThrTrpVal

1225 CACTACATCGCCGCCGAGGAGGAGGACTGGGACTACGCCCCCTGGTGTGGCCCCCGACGACCGCAGCTAC
403▶ HisTyrIleAlaAlaGluGluGluAspTrpAspTyrAlaProLeuValLeuAlaProAspAspArgSerTyr

EagI

1297 AAGAGCCAGTACCTGAACAACGGCCCCCAGCGCATCGGCCGCAAGTACAAGAAGGTGCGCTTCATGGCCTAC
427▶ LysSerGlnTyrLeuAsnAsnGlyProGlnArgIleGlyArgLysTyrLysLysValArgPheMetAlaTyr

Apal

1369 ACCGACGAGACCTTCAAGACCCGCGAGGCCATCCAGCACGAGAGCGGCATCCTGGGCCCCCTGCTGTACGGC
451▶ ThrAspGluThrPheLysThrArgGluAlaIleGlnHisGluSerGlyIleLeuGlyProLeuLeuTyrGly

FIG. 9A

1441 GAGGTGGGCGACACCCTGCTGATCATCTTCAAGAACCAGGCCAGCCGCCCTACAACATCTACCCCCACGGC
475▶ GluValGlyAspThrLeuLeuIleIlePheLysAsnGlnAlaSerArgProTyrAsnIleTyrProHisGly
1513 ATCACCAGCGTGC GCCCCTGTACAGCCGCCCTGCCAAGGGCGTGAAGCACCTGAAGGACTTCCCCATC
499▶ IleThrAspValArgProLeuTyrSerArgArgLeuProLysGlyValLysHisLeuLysAspPheProIle

BglII

1585 CTGCCCCGGCGAGATCTTCAAGTACAAGTGGACCGTGACCGTGGAGGACGGCCCCACCAAGAGCGACCCCCGC
523▶ LeuProGlyGluIlePheLysTyrLysTrpThrValThrValGluAspGlyProThrLysSerAspProArg
1657 TGCCTGACCCGCTACTACAGCAGCTTCGTGAACATGGAGCGCGACCTGGCCAGCGGCCTGATCGGCCCCCTG
547▶ CysLeuThrArgTyrTyrSerSerPheValAsnMetGluArgAspLeuAlaSerGlyLeuIleGlyProLeu
1729 CTGATCTGCTACAAGGAGAGCGTGGACCAGCGCGCAACCAGATCATGAGCGACAAGCGCAACGTGATCCTG
571▶ LeuIleCysTyrLysGluSerValAspGlnArgGlyAsnGlnIleMetSerAspLysArgAsnValIleLeu

KpnI

1801 TTCAGCGTGTTCGACGAGAACCGCAGCTGGTACCTGACCGAGAACATCCAGCGCTTCCTGCCAACCCCGCC
595▶ PheSerValPheAspGluAsnArgSerTrpTyrLeuThrGluAsnIleGlnArgPheLeuProAsnProAla
1873 GGCGTGACGCTGGAGGACCCCGAGTTCCAGGCCAGCAACATCATGCACAGCATCAACGGCTACGTGTTCGAC
619▶ GlyValGlnLeuGluAspProGluPheGlnAlaSerAsnIleMetHisSerIleAsnGlyTyrValPheAsp
1945 AGCCTGCAGCTGAGCGTGTGCCTGCACGAGGTGGCCTACTGGTACATCCTGAGCATCGGCGCCAGACCGAC
643▶ SerLeuGlnLeuSerValCysLeuHisGluValAlaTyrTrpTyrIleLeuSerIleGlyAlaGlnThrAsp
2017 TTCCTGAGCGTGTCTTCAGCGCTACACCTTCAAGCACAAGATGGTGTACGAGGACACCCTGACCCTGTTC
667▶ PheLeuSerValPhePheSerGlyTyrThrPheLysHisLysMetValTyrGluAspThrLeuThrLeuPhe

BamHI

2089 CCCTTCAGCGGCGAGACCGTGTTCATGAGCATGGAGAACCCCGGCTGTGGATCCTGGGCTGCCACAACAGC
691▶ ProPheSerGlyGluThrValPheMetSerMetGluAsnProGlyLeuTrpIleLeuGlyCysHisAsnSer
2161 GACTTCCGCAACCGCGGCATGACCGCCCTGCTGAAGGTGAGCAGCTGCGACAAGAACACCGGCGACTACTAC
715▶ AspPheArgAsnArgGlyMetThrAlaLeuLeuLysValSerSerCysAspLysAsnThrGlyAspTyrTyr
2233 GAGGACAGCTACGAGGACATCAGCGCTACCTGCTGAGCAAGAACAACGCCATCGAGCCCCGCGAGGCGCAGG
739▶ GluAspSerTyrGluAspIleSerAlaTyrLeuLeuSerLysAsnAsnAlaIleGluProArgArgArgArg

BstXI

2305 CGCGAGATCACCCGCACCACCTGCAGAGCGACCAGGAGGAGATCGACTACGACGACACCATCAGCGTGGAG
763▶ ArgGluIleThrArgThrThrLeuGlnSerAspGlnGluGluIleAspTyrAspAspThrIleSerValGlu
2377 ATGAAGAAGGAGGACTTCGACATCTACGACGAGGACGAGAACCAGAGCCCCCGCAGCTTCCAGAAGAAGACC
787▶ MetLysLysGluAspPheAspIleTyrAspGluAspGluAsnGlnSerProArgSerPheGlnLysLysThr

PmlI

2449 CGCCACTACTTCATCGCCGCCGTGGAGCGCCTGTGGGACTACGGCATGAGCAGCAGCCCCACGTGCTGCCG
811▶ ArgHisTyrPheIleAlaAlaValGluArgLeuTrpAspTyrGlyMetSerSerSerProHisValLeuArg
2521 AACCGCGCCCAGAGCGGCAGCGTGCCCCAGTTCAAGAAGGTGGTGTTCAGGAGTTCACCGACGGCAGCTTC
835▶ AsnArgAlaGlnSerGlySerValProGlnPheLysLysValValPheGlnGluPheThrAspGlySerPhe

Apal

2593 ACCCAGCCCCCTGTACCGCGGCGAGCTGAACGAGCACCTGGGCCTGCTGGGCCCCCTACATCCGCGCCGAGGTG
859▶ ThrGlnProLeuTyrArgGlyGluLeuAsnGluHisLeuGlyLeuLeuGlyProTyrIleArgAlaGluVal

BstEII

2665 GAGGACAACATCATGGTGACCTTCCGCAACCAGGCCAGCCGCCCTACAGCTTCTACAGCAGCCTGATCAGC
883▶ GluAspAsnIleMetValThrPheArgAsnGlnAlaSerArgProTyrSerPheTyrSerSerLeuIleSer
2737 TACGAGGAGGACGACGCCAGGGCGCCGAGCCCCGCAAGAACTTCGTGAAGCCCAACGAGACCAAGACCTAC
907▶ TyrGluGluAspGlnArgGlnGlyAlaGluProArgLysAsnPheValLysProAsnGluThrLysThrTyr
2809 TTCTGGAAGGTGCAGCACCACATGGCCCCCACCAGGACGAGTTCGACTGCAAGGCCTGGGCTACTTCAGC
931▶ PheTrpLysValGlnHisHisMetAlaProThrLysAspGluPheAspCysLysAlaTrpAlaTyrPheSer

FIG. 9B

2881 GACGTGGACCTGGAGAAGGACGTGCACAGCGGCCTGATCGGCCCCCTGCTGGTGTGCCACACCAACACCCTG
955▶ AspValAspLeuGluLysAspValHisSerGlyLeuIleGlyProLeuLeuValCysHisThrAsnThrLeu
EagI BstEII

2953 AACCCCGCCCCACGGCCGCCAGGTGACCGTGACGAGTTCGCCCTGTTCTTCACCATCTTCGACGAGACCAAG
979▶ AsnProAlaHisGlyArgGlnValThrValGlnGluPheAlaLeuPhePheThrIlePheAspGluThrLys
3025 AGCTGGTACTTCACCGAGAACATGGAGCGCAACTGCCCGCCCCCTGCAACATCCAGATGGAGGACCCACCC
1003▶ SerTrpTyrPheThrGluAsnMetGluArgAsnCysArgAlaProCysAsnIleGlnMetGluAspProThr
3097 TTCAAGGAGAACTACCGCTTCCACGCCATCAACGGCTACATCATGGACACCCTGCCCGGCCTGGTGATGGCC
1027▶ PheLysGluAsnTyrArgPheHisAlaIleAsnGlyTyrIleMetAspThrLeuProGlyLeuValMetAla
KpnI

3169 CAGGACCAGCGCATCCGCTGGTACCTGCTGAGCATGGGCAGCAACGAGAACATCCACAGCATCCACTTCAGC
1051▶ GlnAspGlnArgIleArgTrpTyrLeuLeuSerMetGlySerAsnGluAsnIleHisSerIleHisPheSer
PmlI

3241 GGCCACGTGTTACCGTGCGCAAGAAGGAGGAGTACAAGATGGCCCTGTACAACCTGTACCCCGGCGTGTTTC
1075▶ GlyHisValPheThrValArgLysLysGluGluTyrLysMetAlaLeuTyrAsnLeuTyrProGlyValPhe
3313 GAGACCGTGGAGATGCTGCCCAGCAAGGCCGGCATCTGGCGCGTGGAGTGCCTGATCGGCGAGCACCTGCAC
1099▶ GluThrValGluMetLeuProSerLysAlaGlyIleTrpArgValGluCysLeuIleGlyGluHisLeuHis
3385 GCCGGCATGAGCACCCCTGTTCTCTGGTGTACAGCAACAAGTCCAGACCCCCCTGGGCATGGCCAGCGGCCAC
1123▶ AlaGlyMetSerThrLeuPheLeuValTyrSerAsnLysCysGlnThrProLeuGlyMetAlaSerGlyHis
ApaI

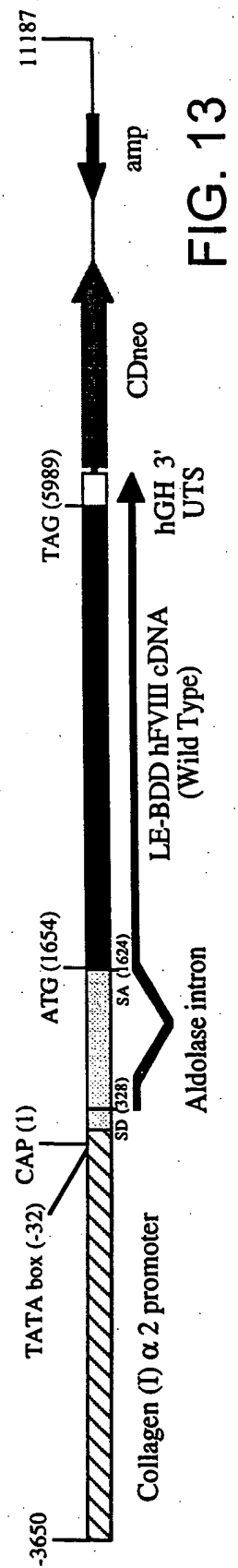
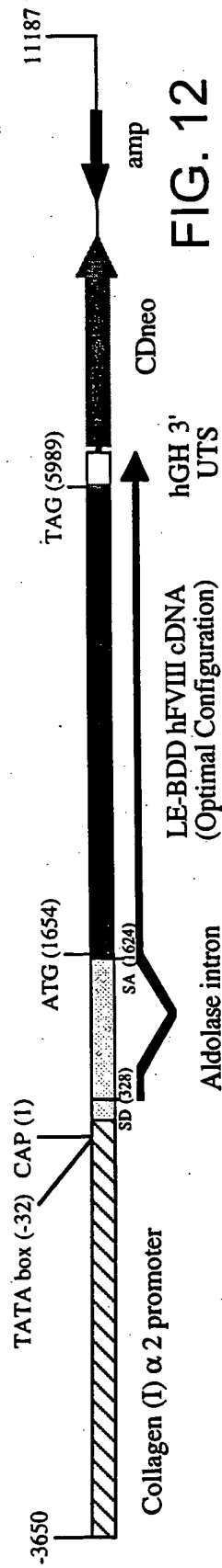
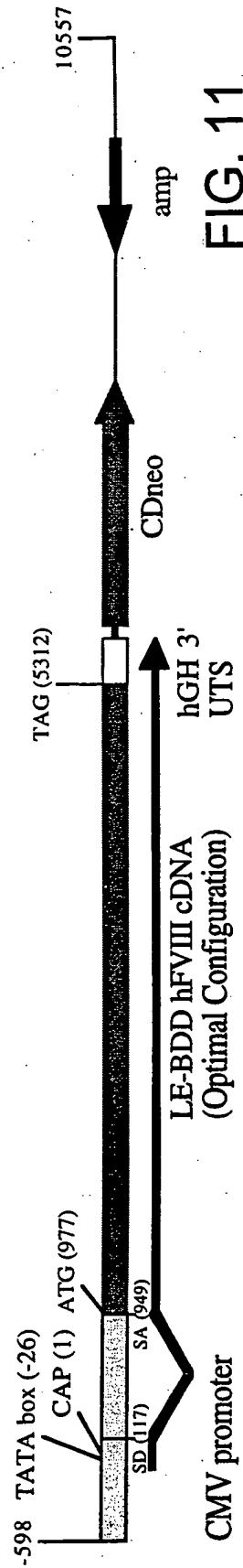
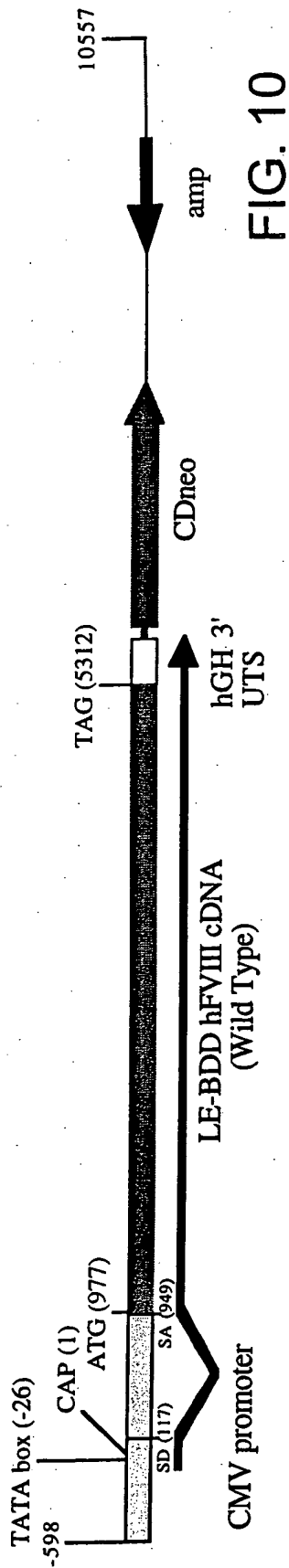
3457 ATCCGCGACTTCCAGATCACCGCCAGCGGCCAGTACGGCCAGTGGGCCCCCAAGCTGGCCCGCTGCACTAC
1147▶ IleArgAspPheGlnIleThrAlaSerGlyGlnTyrGlyGlnTrpAlaProLysLeuAlaArgLeuHisTyr
3529 AGCGGCAGCATCAACGCCTGGAGCACCAGGAGCCCTTCAGCTGGATCAAGGTGGACCTGCTGGCCCCCATG
1171▶ SerGlySerIleAsnAlaTrpSerThrLysGluProPheSerTrpIleLysValAspLeuLeuAlaProMet
3601 ATCATCCACGGCATCAAGACCCAGGGCGCCCGCCAGAAGTTCAGCAGCCTGTACATCAGCCAGTTCATCATC
1195▶ IleIleHisGlyIleLysThrGlnGlyAlaArgGlnLysPheSerSerLeuTyrIleSerGlnPheIleIle
3673 ATGTACAGCCTGGACGGCAAGAAGTGGCAGACCTACCGCGGCAACAGCACCGGCACCCTGATGGTGTCTTCTC
1219▶ MetTyrSerLeuAspGlyLysLysTrpGlnThrTyrArgGlyAsnSerThrGlyThrLeuMetValPhePhe
(SmaI/EcoRV)

3745 GGCAACGTGGACAGCAGCGGCATCAAGCACAAACATCTTCAACCCCCCATCATCGCCCGCTACATCCGCCTG
1243▶ GlyAsnValAspSerSerGlyIleLysHisAsnIlePheAsnProProIleIleAlaArgTyrIleArgLeu
3817 CACCCCAACCACTACAGCATCCGCAGCACCCCTGCGCATGGAGCTGATGGGCTGCGACCTGAACAGCTGCAGC
1267▶ HisProThrHisTyrSerIleArgSerThrLeuArgMetGluLeuMetGlyCysAspLeuAsnSerCysSer
3889 ATGCCCCCTGGGCATGGAGAGCAAGGCCATCAGCGACGCCCAGATCACCGCCAGCAGCTACTTCACCAACATG
1291▶ MetProLeuGlyMetGluSerLysAlaIleSerAspAlaGlnIleThrAlaSerSerTyrPheThrAsnMet
3961 TTCGCCACCTGGAGCCCCAGCAAGGCCCGCCTGCACCTGCAGGGCCGAGCAACGCCTGGCGCCCCCAGGTG
1315▶ PheAlaThrTrpSerProSerLysAlaArgLeuHisLeuGlnGlyArgSerAsnAlaTrpArgProGlnVal
BstEII

4033 AACAAACCCCAAGGAGTGGCTGCAGGTGGACTTCCAGAAGACCATGAAGGTGACCGGCGTGACCACCCAGGGC
1339▶ AsnAsnProLysGluTrpLeuGlnValAspPheGlnLysThrMetLysValThrGlyValThrThrGlnGly
4105 GTGAAGAGCCTGCTGACCAGCATGTACGTGAAGGAGTTCCTGATCAGCAGCAGCCAGGACGGCCACCACTGG
1363▶ ValLysSerLeuLeuThrSerMetTyrValLysGluPheLeuIleSerSerSerGlnAspGlyHisGlnTrp
4177 ACCCTGTTCTTCCAGAACGGCAAGGTGAAGGTGTTCCAGGGCAACCAGGACAGCTTACCCCCGTGGTGAAC
1387▶ ThrLeuPhePheGlnAsnGlyLysValLysValPheGlnGlyAsnGlnAspSerPheThrProValValAsn
4249 AGCCTGGACCCCCCTGCTGACCCGCTACCTGCGCATCCACCCCCAGAGCTGGGTGCACCAGATCGCCCTG
1411▶ SerLeuAspProProLeuLeuThrArgTyrLeuArgIleHisProGlnSerTrpValHisGlnIleAlaLeu
SmaI HindIII

4321 CGCATGGAGGTGCTGGGCTGCGAGGCCAGGACCTGTACTAGCTGCCCGGGCTACAAGCTTTAC
1435▶ ArgMetGluValLeuGlyCysGluAlaGlnAspLeuTyr...

FIG. 9C



Codon Frequency in Highly Expressed Human Genes

% occurrence			% occurrence			% occurrence		
<u>Glu</u>			<u>Cys</u>			<u>Gln</u>		
GA	A	25	TG	C	68	CA	A	12
	G	75		T	32		G	88
<u>Arg</u>			<u>Ala</u>			<u>Gly</u>		
CG	C	37	GC	C	53	GG	C	50
	T	7		T	17		T	12
	A	6		A	13		A	14
	G	21		G	17		G	24
AG	A	10						
	G	18						
<u>Leu</u>			<u>Ser</u>			<u>Pro</u>		
CT	C	26	TC	C	28	CC	C	48
	T	5		T	13		T	19
	A	3		A	5		A	16
	G	58		G	9		G	17
TT	A	2	AG	C	34			
	G	6		T	10			

FIG. 14A

Codon Frequency in Highly Expressed Human Genes

% occurrence			% occurrence			% occurrence		
<u>Ile</u>			<u>Thr</u>			<u>Val</u>		
AT	C	77	AC	C	57	GT	C	25
	T	18		T	14		T	7
	A	5		A	14		A	5
				G	15		G	64
<u>Tyr</u>			<u>Phe</u>			<u>Lys</u>		
TA	C	74	TT	C	80	AA	A	18
	T	26		T	20		G	82
<u>Asn</u>			<u>His</u>					
AA	C	78	CA	C	79			
	T	25		T	21			

FIG. 14B

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